

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/494,585

DATE: 08/15/2001
TIME: 12:29:51

Input Set : A:\Cura57U1.APP
Output Set: N:\CRF3\08152001\I494585.raw

ENTERED

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3 <110> APPLICANT: Shimkets, Richard A
4      Prayaga, Sudhirdas K
6 <120> TITLE OF INVENTION: Novel Fibroblast Growth Factor and Nucleic Acids
7      Encoding Same
9 <130> FILE REFERENCE: 15966-557 FGF-CX
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/494,585
C--> 12 <141> CURRENT FILING DATE: 2001-01-31
14 <150> PRIOR APPLICATION NUMBER: USSN 60/145,899
15 <151> PRIOR FILING DATE: 1999-07-27
17 <160> NUMBER OF SEQ ID NOS: 13
19 <170> SOFTWARE: PatentIn Ver. 2.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 633
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (1)..(633)
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33   1           5           10          15
35 ttg ggc cag cag gtg ggt tcg cat ttc ctg ttg cct cct gcc ggg gag    96
36 Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu Pro Pro Ala Gly Glu
37   20          25          30
39 cgg ccg ccg ctg ctg ggc gag cgc agg agc gcg gcg gag cgg agc gcg    144
40 Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg Ser Ala
41   35          40          45
43 cgc ggc ggg ccg ggg gct gcg cag ctg gcg cac ctg cac ggc atc ctg
44 Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly Ile Leu
45   50          55          60
47 cgc cgc cgg cag ctc tat tgc cgc acc ggc ttc cac ctg cag atc ctg    240
48 Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu
49   65          70          75          80
51 ccc gac ggc agc gtg cag ggc acc cgg cag gac cac agc ctc ttc ggt    288
52 Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly
53   85          90          95
55 atc ttg gaa ttc atc agt gtg gca gtg gga ctg gtc agt att aga ggt    336
56 Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly
57   100         105         110
59 gtg gac agt ggt ctc tat ctt gga atg aat gac aaa gga gaa ctc tat    384
60 Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr
61   115         120         125
63 gga tca gag aaa ctt act tcc gaa tgc atc ttt agg gag cag ttt gaa    432
64 Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu
65   130         135         140
67 gag aac tgg tat aac acc tat tca tct aac ata tat aaa cat gga gac    480

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68	Glu	Asn	Trp	Tyr	Asn	Thr	Tyr	Ser	Ser	Asn	Ile	Tyr	Lys	His	Gly	Asp	
69	145										150		155		160		
71	act	ggc	cgc	agg	tat	ttt	gtg	gca	ctt	aac	aaa	gac	gga	act	cca	aga	528
72	Thr	Gly	Arg	Arg	Tyr	Phe	Val	Ala	Leu	Asn	Lys	Asp	Gly	Thr	Pro	Arg	
73											165		170		175		
75	gat	ggc	gcc	agg	tcc	aag	agg	cat	cag	aaa	ttt	aca	cat	ttc	tta	cct	576
76	Asp	Gly	Ala	Arg	Ser	Lys	Arg	His	Gln	Lys	Phe	Thr	His	Phe	Leu	Pro	
77											180		185		190		624
79	aga	cca	gtg	gat	cca	gaa	aga	gtt	cca	gaa	ttg	tac	aag	gac	cta	ctg	
80	Arg	Pro	Val	Asp	Pro	Glu	Arg	Val	Pro	Glu	Leu	Tyr	Lys	Asp	Leu	Leu	
81											195		200		205		633
83	atg	tac	act														
84	Met	Tyr	Thr								210						
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95	1					5				10				15			
97	Leu	Gly	Gln	Gln	Val	Gly	Ser	His	Phe	Leu	Leu	Pro	Pro	Ala	Gly	Glu	
98						20				25				30			
100	Arg	Pro	Pro	Leu	Leu	Gly	Glu	Arg	Arg	Ser	Ala	Ala	Glu	Arg	Ser	Ala	
101						35				40				45			
103	Arg	Gly	Gly	Pro	Gly	Ala	Ala	Gln	Leu	Ala	His	Leu	His	Gly	Ile	Leu	
104						50				55				60			
106	Arg	Arg	Arg	Gln	Leu	Tyr	Cys	Arg	Thr	Gly	Phe	His	Leu	Gln	Ile	Leu	
107						65				70				75			80
109	Pro	Asp	Gly	Ser	Val	Gln	Gly	Thr	Arg	Gln	Asp	His	Ser	Leu	Phe	Gly	
110						85				90				95			
112	Ile	Leu	Glu	Phe	Ile	Ser	Val	Ala	Val	Gly	Leu	Val	Ser	Ile	Arg	Gly	
113						100				105				110			
115	Val	Asp	Ser	Gly	Leu	Tyr	Leu	Gly	Met	Asn	Asp	Lys	Gly	Glu	Leu	Tyr	
116						115				120				125			
118	Gly	Ser	Glu	Lys	Leu	Thr	Ser	Glu	Cys	Ile	Phe	Arg	Glu	Gln	Phe	Glu	
119						130				135				140			
121	Glu	Asn	Trp	Tyr	Asn	Thr	Tyr	Ser	Ser	Asn	Ile	Tyr	Lys	His	Gly	Asp	
122						145				150				155			160
124	Thr	Gly	Arg	Arg	Tyr	Phe	Val	Ala	Leu	Asn	Lys	Asp	Gly	Thr	Pro	Arg	
125						165				170				175			
127	Asp	Gly	Ala	Arg	Ser	Lys	Arg	His	Gln	Lys	Phe	Thr	His	Phe	Leu	Pro	
128						180				185				190			
130	Arg	Pro	Val	Asp	Pro	Glu	Arg	Val	Pro	Glu	Leu	Tyr	Lys	Asp	Leu	Leu	
131						195				200				205			
133	Met	Tyr	Thr														
134			210														
138	<210>	SEQ ID NO:	3														
139	<211>	LENGTH:	38														

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140 <212> TYPE: DNA
141 <213> ORGANISM: Artificial Sequence
143 <220> FEATURE:
144 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
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151 <211> LENGTH: 34
152 <212> TYPE: DNA
153 <213> ORGANISM: Artificial Sequence
155 <220> FEATURE:
156 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
158 <400> SEQUENCE: 4
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163 <211> LENGTH: 424
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165 <213> ORGANISM: Homo sapiens
167 <400> SEQUENCE: 5
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169 tagaaatctt ccccaatggt actatccagg g aaccaggaa agaccacagc cgattttggca 120
170 ttcttggatt tatcagtata gca gttggcc tggtcagcat tcgaggcgtg gacagtggac 180
171 tctacctcg gatgaatgag a a gggggagc t gttatggatc agaaaaacta acccaagagt 240
172 gtgtatttcag agaacagttc g a a gaaaact ggtataatac gtactcgta aacctatata 300
173 agcacgtgga cactgaaagg c gatactatg ttgcattaaa taaagatggg accccgagag 360
174 aagggactag gactaaacgg caccagaaat tcacacattt ttacactaga ccagtggacc 420
175 ccga 424
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181 <213> ORGANISM: Homo sapiens
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185 ggtggaa ggc ggtggccaa tagagctgcc ggcgcgcagg atgcccgtca ggtgcgccag 120
186 ctgcgcagcc cccggccccgc cgcgcgcgt c cgcctccgccc ggcgcctctgc gtcgcccag 180
187 cagccggcggc cgctccccgg caggaggcaa caggaaatgc gaaaccaccc gtcggcccaa 240
188 gcccctccagg cccggccagaa agcccccgcac ttccggctaag ggagccat 288
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192 <211> LENGTH: 255
193 <212> TYPE: DNA
194 <213> ORGANISM: Homo sapiens
196 <400> SEQUENCE: 7
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198 taagaaaatgt gtaaaattctt gatgccttt ggacctggcg ccatctctt g gatccgtc 120
199 tttgttaatg gccacaaaat acctgcggcc agtgtctcca ttttatata ttttagatga 180
200 ataggtgtta taccaggttt cttcaaactg ctcctaaag atgcattcgg aagtaagtt 240
201 ctcctgaaag agaga 255
204 <210> SEQ ID NO: 8
205 <211> LENGTH: 106

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206 <212> TYPE: DNA
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215 <211> LENGTH: 208
216 <212> TYPE: PRT
217 <213> ORGANISM: HOMO sapiens
219 <400> SEQUENCE: 9
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222 Val Pro Phe Gly Asn Val Pro Val Leu Pro Val Asp Ser Pro Val Leu
223 20 25 30
224 Leu Ser Asp His Leu Gly Gln Ser Glu Ala Gly Gly Leu Pro Arg Gly
225 35 40 45
226 Pro Ala Val Thr Asp Leu Asp His Leu Lys Gly Ile Leu Arg Arg Arg
227 50 55 60
228 Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Glu Ile Phe Pro Asn Gly
229 65 70 75 80
230 Thr Ile Gln Gly Thr Arg Lys Asp His Ser Arg Phe Gly Ile Leu Glu
231 85 90 95
232 Phe Ile Ser Ile Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser
233 100 105 110
234 Gly Leu Tyr Leu Gly Met Asn Glu Lys Gly Glu Leu Tyr Gly Ser Glu
235 115 120 125
236 Lys Leu Thr Gln Glu Cys Val Phe Arg Glu Gln Phe Glu Glu Asn Trp
237 130 135 140
238 Tyr Asn Thr Tyr Ser Ser Asn Leu Tyr Lys His Val Asp Thr Gly Arg
239 145 150 155 160
240 Arg Tyr Tyr Val Ala Leu Asn Lys Asp Gly Thr Pro Arg Glu Gly Thr
241 165 170 175
242 Arg Thr Lys Arg His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val
243 180 185 190
244 Asp Pro Asp Lys Val Pro Glu Leu Tyr Lys Asp Ile Leu Ser Gln Ser
245 195 200 205
246 <210> SEQ ID NO: 10
247 <211> LENGTH: 208
248 <212> TYPE: PRT
249 <213> ORGANISM: Mus sp.
250 <400> SEQUENCE: 10
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252 1 5 10 15
253 Val Pro Phe Gly Asn Val Pro Val Leu Pro Val Asp Ser Pro Val Leu
254 20 25 30
255 Leu Asn Asp His Leu Gly Gln Ser Glu Ala Gly Gly Leu Pro Arg Gly
256 35 40 45
257 Pro Ala Val Thr Asp Leu Asp His Leu Lys Gly Ile Leu Arg Arg Arg
258 50 55 60
259

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281 Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Glu Ile Phe Pro Asn Gly
 282 65 70 75 80
 284 Thr Ile Gln Gly Thr Arg Lys Asp His Ser Arg Phe Gly Ile Leu Glu
 285 85 90 95
 287 Phe Ile Ser Ile Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser
 288 100 105 110
 290 Gly Leu Tyr Leu Gly Met Asn Glu Lys Gly Glu Leu Tyr Gly Ser Glu
 291 115 120 125
 293 Lys Leu Thr Gln Glu Cys Val Phe Arg Glu Gln Phe Glu Glu Asn Trp
 294 130 135 140
 296 Tyr Asn Thr Tyr Ser Ser Asn Leu Tyr Lys His Val Asp Thr Gly Arg
 297 145 150 155 160
 299 Arg Tyr Tyr Val Ala Leu Asn Lys Asp Gly Thr Pro Arg Glu Gly Thr
 300 165 170 175
 302 Arg Thr Lys Arg His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val
 303 180 185 190
 305 Asp Pro Asp Lys Val Pro Glu Leu Tyr Lys Asp Ile Leu Ser Gln Ser
 306 195 200 205
 312 <210> SEQ ID NO: 11
 313 <211> LENGTH: 208
 314 <212> TYPE: PRT
 315 <213> ORGANISM: Rattus sp.
 317 <400> SEQUENCE: 11
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 319 1 5 10 15
 321 Val Pro Phe Gly Asn Val Pro Val Leu Pro Val Asp Ser Pro Val Leu
 322 20 25 30
 324 Leu Ser Asp His Leu Gly Gln Ser Glu Ala Gly Gly Leu Pro Arg Gly
 325 35 40 45
 327 Pro Ala Val Thr Asp Leu Asp His Leu Lys Gly Ile Leu Arg Arg Arg
 328 50 55 60
 330 Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Glu Ile Phe Pro Asn Gly
 331 65 70 75 80
 333 Thr Ile Gln Gly Thr Arg Lys Asp His Ser Arg Phe Gly Ile Leu Glu
 334 85 90 95
 336 Phe Ile Ser Ile Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser
 337 100 105 110
 339 Gly Leu Tyr Leu Gly Met Asn Glu Lys Gly Glu Leu Tyr Gly Ser Glu
 340 115 120 125
 342 Lys Leu Thr Gln Glu Cys Val Phe Arg Glu Gln Phe Glu Glu Asn Trp
 343 130 135 140
 345 Tyr Asn Thr Tyr Ser Ser Asn Leu Tyr Lys His Val Asp Thr Gly Arg
 346 145 150 155 160
 348 Arg Tyr Tyr Val Ala Leu Asn Lys Asp Gly Thr Pro Arg Glu Gly Thr
 349 165 170 175
 351 Arg Thr Lys Arg His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val
 352 180 185 190
 354 Asp Pro Asp Lys Val Pro Glu Leu Tyr Lys Asp Ile Leu Ser Gln Ser
 355 195 200 205

VERIFICATION SUMMARY

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Input Set : A:\Cura57Ul.APP

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date